

ATTACHMENT A

<110> APPLICANT: Better, Marc D.  
 Horwitz, Arnold H.  
 <120> TITLE OF INVENTION: Human Engineered to Antibodies to Ep-CAM  
 <130> FILE REFERENCE: 14923US02  
 <140> CURRENT APPLICATION NUMBER: US/10/816,276  
 <141> CURRENT FILING DATE: 2004-03-31  
 <150> PRIOR APPLICATION NUMBER: 60/459,334  
 <151> PRIOR FILING DATE: 2003-03-31  
 <160> NUMBER OF SEQ ID NOS: 59  
 <170> SOFTWARE: PatentIn version 3.2

<210> 1  
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 <212> DNA  
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 <221> misc\_feature  
 <223> Mouse Human Chimeric Light Chain DNA and Protein  
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ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aag	192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
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Ser Gly Val Pro Asp Arg Phe Ser Ser Gly Ser Gly Thr Asp Phe	
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Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
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Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys	
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Thr Leu Arg	Ile Ser Arg	Val Glu Ala	Glu Asp Val	Gly Val Tyr	Tyr
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<221> misc\_feature

<223> Mouse-Human chimeric Heavy Chain DNA and Protein Sequence

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Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly	
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Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly	
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130 135 140	
ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg	528
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Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser	
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Lys															

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<223> Variable Region of the Light Chain is Amino Acids 1-112

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Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
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<221> misc\_feature

<223> Low + Moderate Risk Human Engineered ING-1 Light Chain (LC)

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<222> (61)..()

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-20          -15          -10          -5
gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc ctg cca      96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
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Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
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cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
45					50					55					60	
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
				65				70						75		
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
		80					85					90				
tgt	gct	cag	aac	cta	gag	ctt	cca	cgg	acg	ttc	ggg	cag	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
	95					100					105					
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
	110				115						120					
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
125				130				135						140		
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
			145					150						155		
aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
		160				165					170					
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
	175					180					185					
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	
	190				195					200						
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag	720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		
205				210					215							

<210> 8

<211> 239

<212> PRT

<213> Homo Sapiens

<400> 8

Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Val	Leu	Trp	Ile	Pro	
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Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	
		-1	1				5					10				
Val	Thr	Pro	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
	15					20					25					
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
30					35					40						
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
45				50					55					60		
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
			65					70					75			
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
		80					85					90				
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
	95						100					105				

Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
110						115					120				
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
125					130					135					140
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
				145					150					155	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
			160					165					170		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		175					180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	190					195					200				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
205					210					215					

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<210> 9
<211> 88
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> KL1 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)
<400> 9
      tgtcgacacc atgaggttct ctgctcagct tctggggctg cttgtgctct ggatccctgg      60
      atccactgca gacatcgtga tgaccacg                                     88

<210> 10
<211> 85
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> KL2 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)
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      actottacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag      60
      tgcagactgg gtcacacga tgtct                                         85

<210> 11
<211> 88
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
<223> KL3 V Region Oligos Human Engineered ING-1 Light Chain (Kappa
low)
<400> 11
      ctgccggtct agtaagagtc tcctacatag taatggcatc acttatttgt attggtatct      60
      gcagaaacca gggcagtctc ctcagctg                                     88

<210> 12
<211> 86
<212> DNA
<213> Homo Sapiens
<220>
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<223> KL4 V Region Oligos Human Engineered ING-1 Light Chain (Kappa  
 low)  
 <400> 12  
 tgtcccagat ccactgctac tgaacctgtc tgggaccctt gaggtctctg tagacatctg 60  
 atagatgagc agctgaggag actgcc 86

<210> 13  
 <211> 77  
 <212> DNA  
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 <220>  
 <221> misc\_feature  
 <223> KL5 V Region Oligos Human Engineered ING-1 Light Chain (Kappa  
 low)  
 <400> 13  
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 ggagtttatt actgtgc 77

<210> 14  
 <211> 75  
 <212> DNA  
 <213> Homo Sapiens  
 <220>  
 <221> misc\_feature  
 <223> KL6 V Region Oligos Human Engineered ING-1 Light Chain (Kappa  
 low)  
 <400> 14  
 tttgatttca agcttggtgc cctgaccgaa cgtccgtgga agctctaggt tctgagcaca 60  
 gtaataaact cccac 75

<210> 15  
 <211> 22  
 <212> DNA  
 <213> Homo Sapiens  
 <220>  
 <221> misc\_feature  
 <223> Low Risk Primers Forward Primer: KF ING-1 Light Chain Oligos  
 <400> 15  
 ttatgtcgac accatgaggt tc 22

<210> 16  
 <211> 21  
 <212> DNA  
 <213> Homo Sapiens  
 <220>  
 <221> misc\_feature  
 <223> Low risk Primers Reverse Primer: KR ING-1 Light Chain Oligos  
 <400> 16  
 tttgatttca agcttggtgc c 21

<210> 17  
 <211> 85  
 <212> DNA  
 <213> Homo Sapiens  
 <220>  
 <221> misc\_feature  
 <223> Moderate Risk Primer: KM2 V Region Oligos Human Engineered ING-1

Light Chain Oligos (Kappa Moderate)

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<400> 17
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tggagactgg gtcacacga tgtct                                           85

<210> 18
<211> 1398
<212> DNA
<213> Homo Sapiens
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<221> misc_feature
<223> Low Risk Human Engineered ING-1 Heavy Chain (HC)
<220>
<221> misc_feature
<223> Variable region of HC is Amino Acids is 1-116
<220>
<221> CDS
<222> (1)..(1395)
<220>
<221> mat_peptide
<222> (58)..()
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Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                                -15                    -10                    -5
gcc caa gca cag atc cag ttg gtg cag tct gga cct gag gtg aag aag      96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
                                -1  1                    5                    10
cct gga gag tcc gtc aag atc tcc tgc aag gct tct gga tat acc ttc      144
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                                15                    20                    25
aca aaa tat gga atg aac ttg gtg aag cag gct cca gga cag ggt tta      192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
30                                35                                40                                45
aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt      240
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
                                50                    55                    60
gat gac ttc aag gga cgg ttt acc ttc acc ttg gac acc tct act agc      288
Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
                                65                    70                    75
act gcc tat ttg gaa atc tct tct ctc cgg agt gag gac acg gct aca      336
Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
                                80                    85                    90
tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga      384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
95                                100                    105
acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc      432
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110                                115                    120                    125
ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg      480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                                130                    135                    140
ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg      528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
                                145                    150                    155
aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta      576
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

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	160		165		170		
cag	tcc	tca	gga	ctc	tac	tcc	ctc
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu
	175					180	
agc	agc	ttg	ggc	acc	cag	acc	tac
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr
	190				195		200
agc	aac	acc	aag	gtg	gac	aag	aga
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg
			210				215
act	cac	aca	tgc	cca	ccg	tgc	cca
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
			225				230
tca	gtc	ttc	ctc	ttc	ccc	cca	aaa
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
	240						245
cgg	acc	cct	gag	gtc	aca	tgc	gtg
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
	255					260	
cct	gag	gtc	aag	ttc	aac	tgg	tac
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
	270				275		280
gcc	aag	aca	aag	ccg	cgg	gag	gag
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
			290				295
gtc	agc	gtc	ctc	acc	gtc	ctg	cac
Val	Ser	Val	Leu	Thr	Val	Leu	His
			305				310
tac	aag	tgc	aag	gtc	tcc	aac	aaa
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
	320					325	
acc	atc	tcc	aaa	gcc	aaa	ggg	cag
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
	335					340	
ctg	ccc	cca	tcc	cgg	gat	gag	ctg
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu
	350				355		360
tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro
			370				375
agc	aat	ggg	cag	ccg	gag	aac	aac
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn
		385				390	
gac	tcc	gac	ggc	tcc	ttc	ttc	ctc
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu
	400					405	
agc	agg	tgg	cag	cag	ggg	aac	gtc
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val
	415					420	
gct	ctg	cac	aac	cac	tac	acg	cag
Ala	Leu	His	Asn	His	Tyr	Thr	Gln
	430				435		
aaa	tga						
Lys							
							440
							445

624  
672  
720  
768  
816  
864  
912  
960  
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<210> 19  
<211> 465

<212> PRT

<213> Homo Sapiens

<400> 19

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	-1	1				5					10					
Pro	Gly	Glu	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
	15				20					25						
Thr	Lys	Tyr	Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
30				35					40						45	
Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Glu	Glu	Pro	Thr	Tyr	Gly	
			50					55						60		
Asp	Asp	Phe	Lys	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser	
		65					70					75				
Thr	Ala	Tyr	Leu	Glu	Ile	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Thr	
	80					85					90					
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly	
	95					100				105						
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
110					115					120					125	
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
				130					135					140		
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
			145					150					155			
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
	160						165					170				
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
	175					180				185						
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
190					195					200					205	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	
			210						215					220		
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	
			225					230						235		
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
	240						245					250				
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	
	255					260				265						
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
270					275					280					285	
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	
				290					295					300		
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
			305					310					315			
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	
	320						325					330				
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	
	335					340				345						
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	
350					355					360					365	
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	
				370					375					380		
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	
			385					390					395			
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	
		400					405					410				

Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
415						420					425				
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly
430					435					440					445
Lys															

<210> 20

<211> 1398

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<223> Low + Moderate Risk Human Engineered ING-1 Heavy Chain (HC)

<220>

<221> CDS

<222> (1)..(1395)

<220>

<221> mat\_peptide

<222> (58)..()

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				-15					-10					-5		
gcc	caa	gca	cag	atc	cag	ttg	gtg	cag	tct	gga	gct	gag	gtg	aag	aag	96
Ala	Gln	Ala	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
	-1	1				5					10					
cct	gga	gag	tca	gtc	aag	atc	tcc	tgc	aag	gct	tct	gga	tat	acc	ttc	144
Pro	Gly	Glu	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
	15				20					25						
aca	aaa	tat	gga	atg	aac	tgg	gtg	cga	cag	gct	cca	gga	caa	ggt	tta	192
Thr	Lys	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
	30			35				40						45		
gag	tgg	atg	ggc	tgg	ata	aac	acc	tac	act	gaa	gag	cca	aca	tat	ggt	240
Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Glu	Glu	Pro	Thr	Tyr	Gly	
			50					55						60		
cag	aag	ttc	cag	gga	cgg	ttt	acc	ttc	acc	ttg	gac	acc	tct	act	agc	288
Gln	Lys	Phe	Gln	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser	
			65			70							75			
act	gcc	tat	ttg	gaa	atc	tct	tcg	ctc	cgg	agt	gag	gac	acg	gct	gtg	336
Thr	Ala	Tyr	Leu	Glu	Ile	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
	80				85							90				
tat	ttc	tgt	gca	aga	ttt	ggc	tct	gct	gtg	gac	tac	tgg	ggt	caa	gga	384
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly	
	95				100					105						
acc	ttg	gtc	acc	gtc	tcc	tca	gcc	agc	aca	aag	ggc	cca	tcg	gtc	ttc	432
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
	110				115					120				125		
ccc	ctg	gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	480
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
			130					135						140		
ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	528
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
			145				150						155			
aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	576
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
		160				165						170				
cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	624

Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
175						180				185						
agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	672
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
190					195				200					205		
agc	aac	acc	aag	gtg	gac	aag	aga	gtt	gag	ccc	aaa	tct	tgt	gac	aaa	720
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	
				210					215					220		
act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	768
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	
			225					230					235			
tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	816
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
		240					245					250				
cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	864
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	
	255					260				265						
cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	912
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
270					275				280					285		
gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgg	gtg	960
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	
				290				295						300		
gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	1008
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
			305				310						315			
tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	1056
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	
	320					325						330				
acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	1104
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	
	335				340					345						
ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	1152
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	
350				355					360					365		
tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	1200
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	
			370				375						380			
agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	1248
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	
			385				390					395				
gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	1296
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	
	400				405							410				
agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	1344
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	
	415				420					425						
gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	1392
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	
430				435					440					445		
aaa	tga															1398
Lys																

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 <212> PRT  
 <213> Homo Sapiens



<400> 21

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	-1	1				5					10					
Pro	Gly	Glu	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
	15					20					25					
Thr	Lys	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
30					35					40					45	
Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Glu	Glu	Pro	Thr	Tyr	Gly	
			50						55					60		
Gln	Lys	Phe	Gln	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser	
			65					70					75			
Thr	Ala	Tyr	Leu	Glu	Ile	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
	80						85					90				
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly	
	95					100				105						
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
110					115					120					125	
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
				130					135					140		
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
			145					150					155			
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
	160						165					170				
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
	175					180					185					
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
190					195					200					205	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	
			210						215					220		
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	
			225					230					235			
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
	240						245					250				
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	
	255					260				265						
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
270					275					280					285	
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	
				290					295					300		
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
			305					310					315			
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	
	320						325					330				
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	
	335					340						345				
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	
350					355					360					365	
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	
			370						375					380		
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	
			385					390					395			
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	
	400						405					410				
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	
	415					420						425				

Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly
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Lys															

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      ccaagcacag atccagttgg tgcagtctgg a                                91

<210> 23
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<212> DNA
<213> HomoSapiens
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<223> GL2 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 23
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      cttcacctca ggtccagact gcaccaactg                                90

<210> 24
<211> 91
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GL3 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 24
      tggatatacc ttcacaaaat atggaatgaa ctgggtgaag caggctccag gacagggttt      60
      aaagtggatg ggctggataa acacctacac t                                91

<210> 25
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GL4 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
      (gamma low)
<400> 25
      cagtgtagt agaggtgtcc aaggtgaagg taaaccgtcc cttgaagtca tcaccatatg      60
      ttggctcttc agtgtaggtg tttatccage                                91

<210> 26
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<212> DNA
<213> HomoSapiens
<220>

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<221> misc\_feature  
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 (gamma low)  
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 acatatttct gtgcaagatt tggctctgct 90  
  
 <210> 27  
 <211> 85  
 <212> DNA  
 <213> HomoSapiens  
 <220>  
 <221> misc\_feature  
 <223> GL6 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos  
 (gamma low)  
 <400> 27  
 gaccgatggg ccctttgtgc tggctgagga gacggtgacc aaggttcctt gaccccagta 60  
 gtccacagca gagccaaatc ttgca 85  
  
 <210> 28  
 <211> 22  
 <212> DNA  
 <213> HomoSapiens  
 <220>  
 <221> misc\_feature  
 <223> Human Engineered ING-1 Heavy Chain Oligos-Low Risk Primers  
 Forward primer:GF  
 <400> 28  
 ttatgtcgac accatggctt gg 22  
  
 <210> 29  
 <211> 17  
 <212> DNA  
 <213> HomoSapiens  
 <220>  
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 <223> Human Engineered ING-1 Heavy Chain Oligos Low Risk Primers  
 -Reverse Primer GR  
 <220>  
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 <223> ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR  
 <400> 29  
 gaccgatggg ccctttg 17  
  
 <210> 30  
 <211> 90  
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 <223> GM2 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low  
 + Moderate Risk Primers  
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 cttcacctca gctccagact gcaccaactg 90  
  
 <210> 31

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<211> 91
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<220>
<221> misc_feature
<223> GM3 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers
<400> 31
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    agagtggatg ggctggataa acacctacac t                                     91

<210> 32
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<223> GM4 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers
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    ttggtctcttc agtgtagggtg tttatccagc                                     90

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<223> GM5 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
+ Moderate Risk Primers
<400> 33
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    gtgtatttct gtgcaagatt tggctctgct                                     90

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<211> 720
<212> DNA
<213> Homo sapiens
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moderate risk proline change; proline at position 8 (P1)
<220>
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<222> (1)..(717)
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    Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
    -20                -15                -10                -5
    gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca    96
    Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
    -1  1                5                10
    gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt    144

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Val	Thr	Leu	Gly	Glu	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser		
		15					20					25					
ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa		192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys		
		30				35					40						
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc		240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala		
		45			50					55				60			
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc		288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe		
				65					70					75			
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	ggt	tat	tac		336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr		
		80					85					90					
tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggt	cag	ggc	acc	aag		384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys		
		95					100					105					
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg		432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro		
		110				115					120						
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	ggt	gtg	tgc	ctg		480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu		
		125			130					135				140			
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat		528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp		
				145					150					155			
aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac		576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp		
			160					165					170				
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa		624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys		
		175					180					185					
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag		672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln		
		190				195					200						
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag		720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys			
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<210> 35

<211> 239

<212> PRT

<213> Homo sapiens

<400> 35

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Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Asn	Pro		
			-1	1				5					10				
Val	Thr	Leu	Gly	Glu	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser		
		15				20						25					
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys		
		30			35						40						
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala		
		45			50				55					60			
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe		
			65						70					75			
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr		



ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg	432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
aac gcc ctc caa tgc ggt aac tcc cag gag agt gtc aca gag cag gac	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
175 180 185	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
190 195 200	
ggc ctg agc tgc ccc gtc aca aag agc ttc aac agg gga gag tgt tag	720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
205 210 215	

<210> 37

<211> 239

<212> PRT

<213> Homo sapiens

<400> 37

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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro	
-1 1 5 10	
Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser	
15 20 25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
30 35 40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala	
45 50 55 60	
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe	
65 70 75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
80 85 90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	
95 100 105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
175 180 185	
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
190 195 200	
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
205 210 215	

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<210> 38
<211> 720
<212> DNA
<213> Homo sapiens
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      -20                      -15                      -10                      -5
      gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca      96
      Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
                        -1 1                      5                      10
      gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
      Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                        15                      20                      25
      ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
                        30                      35                      40
      cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc      240
      Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
      45                      50                      55                      60
      tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc      288
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                        65                      70                      75
      act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac      336
      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                        80                      85                      90
      tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag      384
      Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                        95                      100                      105
      ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg      432
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
                        110                      115                      120
      cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg      480
      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
      125                      130                      135                      140
      ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat      528
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                        145                      150                      155
      aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac      576
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
                        160                      165                      170
      agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa      624
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
                        175                      180                      185
      gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag      672
      Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln

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190	195	200	
ggc ctg agc tcg ccc gtc	aca aag agc ttc aac	agg gga gag tgt tag	720
Gly Leu Ser Ser Pro Val	Thr Lys Ser Phe Asn	Arg Gly Glu Cys	
205	210	215	

<210> 39  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens  
 <400> 39

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro	
-20	-15 -10 -5
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro	
	-1 1 5 10
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser	
	15 20 25
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
	30 35 40
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala	
	45 50 55 60
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe	
	65 70 75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
	80 85 90
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	
	95 100 105
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
	110 115 120
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
	125 130 135 140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
	145 150 155
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
	160 165 170
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
	175 180 185
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
	190 195 200
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
205	210 215

<210> 40  
 <211> 720  
 <212> DNA  
 <213> Homo sapiens  
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 <223> P1P2=Human Engineered (low risk) ING1 light Chain with one  
 moderate risk proline change; proline at position 8 (P1) 15(P2)  
 <220>  
 <221> CDS  
 <222> (1)..(717)  
 <220>  
 <221> mat\_peptide  
 <222> (61)..()  
 <400> 40

atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct

Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Val	Leu	Trp	Ile	Pro		
-20					-15					-10					-5		
gga	tcc	act	gca	gac	atc	gtg	atg	acc	cag	tct	cca	ctc	tcc	aat	cca	96	
Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Asn	Pro		
			-1	1				5					10				
gtc	act	cct	gga	gag	tca	ggc	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144	
Val	Thr	Pro	Gly	Glu	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser		
		15					20					25					
ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192	
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys		
	30					35					40						
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240	
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala		
45					50					55					60		
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe		
				65				70						75			
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	ggt	tat	tac	336	
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr		
			80					85					90				
tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggc	cag	ggc	acc	aag	384	
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys		
		95					100					105					
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432	
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro		
	110					115					120						
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	ggt	gtg	tgc	ctg	480	
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu		
125					130					135					140		
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528	
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp		
				145					150					155			
aac	gcc	ctc	caa	tcg	ggc	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp		
			160					165					170				
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	624	
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys		
		175					180					185					
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	672	
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln		
	190					195					200						
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag	720	
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys			
205					210					215							

<210> 41  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens  
 <400> 41

Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Val	Leu	Trp	Ile	Pro		
-20					-15					-10					-5		
Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Asn	Pro		
			-1	1				5					10				
Val	Thr	Pro	Gly	Glu	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser		
		15					20					25					
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys		

30	35	40																	
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala				
45					50					55					60				
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe				
				65					70					75					
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr				
			80					85					90						
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys				
	95						100					105							
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro				
110						115					120								
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu				
125					130					135					140				
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp				
				145				150					155						
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp				
			160				165					170							
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys				
	175					180						185							
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln				
190					195					200									
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys					
205				210				215											

<210> 42  
 <211> 720  
 <212> DNA  
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 <223> P1P3= Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 18 (P3)  
 <220>  
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 <222> (1)..(717)  
 <220>  
 <221> mat\_peptide  
 <222> (61)..()  
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Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Val	Leu	Trp	Ile	Pro		
-20				-15				-10				-5				
gga	tcc	act	gca	gac	atc	gtg	atg	acc	cag	tct	cca	ctc	tcc	aat	cca	96
Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Asn	Pro	
			-1	1			5				10					
gtc	act	ctg	gga	gag	ccg	ggc	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144
Val	Thr	Leu	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
	15				20			25								
ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
	30				35			40								
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
45				50				55					60			
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
				65				70					75			

act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac	336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
80 85 90	
tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag	384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	
95 100 105	
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg	432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
175 180 185	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
190 195 200	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag	720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
205 210 215	

<210> 43

<211> 239

<212> PRT

<213> Homo sapiens

<400> 43

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro	
-20 -15 -10 -5	
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro	
-1 1 5 10	
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser	
15 20 25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys	
30 35 40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala	
45 50 55 60	
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe	
65 70 75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
80 85 90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys	
95 100 105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
110 115 120	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
125 130 135 140	
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
145 150 155	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
160 165 170	

Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		175					180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	190					195					200				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
205					210					215					

<210> 44  
 <211> 720  
 <212> DNA  
 <213> Homo sapiens  
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 <221> misc\_feature  
 <223> P2P3=Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 18 (P3)  
 <220>  
 <221> CDS  
 <222> (1)..(717)  
 <220>  
 <221> mat\_peptide  
 <222> (61)..()  
 <400> 44

atg	agg	ttc	tct	gct	cag	ctt	ctg	ggg	ctg	ctt	gtg	ctc	tgg	atc	cct	48
Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Val	Leu	Trp	Ile	Pro	
-20					-15				-10						-5	
gga	tcc	act	gca	gac	atc	gtg	atg	acc	cag	tct	gca	ctc	tcc	aat	cca	96
Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Ala	Leu	Ser	Asn	Pro	
			-1	1				5					10			
gtc	act	cct	gga	gag	ccg	ggt	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144
Val	Thr	Pro	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Ser	Lys	
		15				20						25				
ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
		30				35					40					
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
45					50				55						60	
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
				65					70					75		
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
		80						85					90			
tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggt	cag	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
		95				100						105				
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
		110				115						120				
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
					125					130					140	
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
				145					150					155		
aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	

	160		165		170	
agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa						624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys						
	175		180		185	
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag						672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln						
	190		195		200	
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag						720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys						
205	210		215			

<210> 45

<211> 239

<212> PRT

<213> Homo sapiens

<400> 45

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro						
-20		-15		-10		-5
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro						
	-1	1		5		10
Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser						
	15		20		25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys						
30		35		40		
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala						
45		50		55		60
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe						
	65		70		75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr						
	80		85		90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys						
	95		100		105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro						
	110		115		120	
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu						
125		130		135		140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp						
	145		150		155	
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp						
	160		165		170	
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys						
	175		180		185	
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln						
	190		195		200	
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys						
205	210		215			

<210> 46

<211> 85

<212> DNA

<213> Homo Sapiens

<220>

<221> misc\_feature

<223> P1 Oligo Human Engineered ING-1 with proline oligos

<400> 46

actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag	60
tggagactgg gtcacacga tgtct	85

<210> 47  
 <211> 85  
 <212> DNA  
 <213> Homo Sapiens  
 <220>  
 <221> misc\_feature  
 <223> P2 Oligo Human Engineered ING-1 with proline oligos  
 <400> 47  
 actcttacta gaccggcagg agatggaacc tgactctcca ggagtgactg gattggagag 60  
 tgcagactgg gtcatcacga tgtct 85

<210> 48  
 <211> 85  
 <212> DNA  
 <213> Homo Sapiens  
 <220>  
 <221> misc\_feature  
 <223> P3 Oligo Human Engineered ING-1 with proline oligos  
 <400> 48  
 actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag 60  
 tgcagactgg gtcatcacga tgtct 85

<210> 49  
 <211> 85  
 <212> DNA  
 <213> Homo Sapiens  
 <220>  
 <221> misc\_feature  
 <223> P1P2 Oligo Human Engineered ING-1 with proline oligos  
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      Thr Ala Thr Phe Ala Ala Ala Gln Glu Cys Val Cys Glu Asn Tyr
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      Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
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      act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc
      Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
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      Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
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      aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat
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      cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc
      Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
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      Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
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      Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
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      624

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Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu		
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cct	gaa	ttc	tca	atg	cag	ggg	cta	aaa	taa							798	
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Lys	Leu	Ala	Val	Asn	Cys	Phe	Val	Asn	Asn	Asn	Arg	Gln	Cys	Gln	Cys		
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Arg	Ala	Lys	Pro	Glu	Gly	Ala	Leu	Gln	Asn	Asn	Asp	Gly	Leu	Tyr	Asp		
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Lys	Asp	Thr	Glu	Ile	Thr	Cys	Ser	Glu	Arg	Val	Arg	Thr	Tyr	Trp	Ile		
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Ile	Ile	Glu	Leu	Lys	His	Lys	Ala	Arg	Glu	Lys	Pro	Tyr	Asp	Ser	Lys		
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Ser	Leu	Arg	Thr	Ala	Leu	Gln	Lys	Glu	Ile	Thr	Thr	Arg	Tyr	Gln	Leu		
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Asp	Pro	Lys	Phe	Ile	Thr	Ser	Ile	Leu	Tyr	Glu	Asn	Asn	Val	Ile	Thr		
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Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser		
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Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu		
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Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp	
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Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly	
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Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp	
90 95 100 105	
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Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile	
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125 130 135	
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Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu	
140 145 150	
gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act	576
Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr	
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Val	Val	Val	Val	Ile	Ala	Val	Val	Ala	Gly	Ile	Val	Val	Leu	Val	Ile	
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Ser	Arg	Lys	Lys	Arg	Met	Ala	Lys	Tyr	Glu	Lys	Ala	Glu	Ile	Lys	Glu	
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